

We claim:

1. An engineered nucleic acid molecule comprising:
 - (i) a first stem-forming portion;
 - (ii) a second stem-forming portion, wherein the two stem-forming portions are complementary or substantially complementary, and
 - (iii) a non-stem-forming portion that forms a loop connecting the 3' end of the first stem-forming portion and the 5' end of the second stem-forming portion, wherein the engineered nucleic acid molecule forms a stem-loop structure that represses translation when positioned upstream of an open reading frame (ORF).
2. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule is positioned upstream of the ORF.
3. The nucleic acid molecule of claim 1, wherein the first and second stem-forming portions are substantially complementary.
4. The nucleic acid molecule of claim 1, wherein at least a portion of the first stem-forming portion is complementary or substantially complementary to a ribosome binding site (RBS).
5. The nucleic acid molecule of claim 1, wherein at least a portion of the first stem-forming portion is complementary or substantially complementary to a Kozak consensus sequence.
6. The nucleic acid molecule of claim 1, wherein the sequence of the second stem-forming portion comprises an RBS.
7. The nucleic acid molecule of claim 1, wherein the sequence of the non-stem-forming portion comprises YUNR.
8. The nucleic acid molecule of claim 1, wherein the non-stem forming portion is 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides in length.
9. The nucleic acid molecule of claim 1, wherein the non-stem forming portion is between 13 and 50 nucleotides in length, inclusive.

10. The nucleic acid molecule of claim 1, wherein the length of the stem is between 4 and 100 nucleotides, inclusive.
11. The nucleic acid molecule of claim 1, wherein the length of the stem is between 6 and 50 nucleotides, inclusive.
12. The nucleic acid molecule of claim 1, wherein the length of the stem is between 12 and 30 nucleotides, inclusive.
13. The nucleic acid molecule of claim 1, wherein the length of the stem is approximately 19 nucleotides.
14. The nucleic acid molecule of claim 1, wherein the stem exhibits at least 66% complementarity.
15. The nucleic acid molecule of claim 1, wherein the stem exhibits between 75 and 95% complementarity.
16. The nucleic acid molecule of claim 1, wherein the stem exhibits approximately 85% complementarity.
17. The nucleic acid molecule of claim 1, wherein the stem includes at least one area of non-complementarity.
18. The nucleic acid molecule of claim 17, wherein the stem includes at least one bulge.
19. The nucleic acid molecule of claim 1, wherein the stem includes at least two dispersed areas of non-complementarity.
20. The nucleic acid molecule of claim 19, wherein the stem includes at least two dispersed bulges.
21. The nucleic acid molecule of claim 1, wherein the stem includes at least three dispersed areas of non-complementarity.
22. The nucleic acid molecule of claim 21, wherein the stem includes at least three dispersed bulges.

23. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule forms a single stable stem.
24. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule represses translation in the absence of a ligand.
25. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule is composed of RNA.
26. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule is composed of DNA.
27. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule is composed of DNA and RNA.
28. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule comprises a nucleotide analog.
29. The nucleic acid molecule of claim 1, wherein the first stem-forming portion comprises a sequence complementary or substantially complementary to a sequence in the 5' portion of an ORF.
30. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule comprises a start codon.
31. The nucleic acid molecule of claim 30, wherein the nucleic acid molecule comprises a spacer comprising one or more nucleotides between the 3' end of the second stem-forming portion and the start codon.
32. The nucleic acid molecule of claim 30, wherein all or part of the start codon is located within the second stem-forming portion.
33. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule comprises one or more nucleotides upstream of the 5' end of the first stem-forming portion.
34. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule comprises between 5 and 50 nucleotides upstream of the 5' end of the first stem-forming portion.

35. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule comprises a ligand binding domain.
36. The nucleic acid molecule of claim 1, further comprising a third stem-forming portion that is complementary or substantially complementary to the second stem-forming portion, wherein the first and third stem-forming portions form alternate stem-loop structures with the second stem-forming portion.
37. The nucleic acid molecule of claim 36, wherein the first and third stem-forming portions comprise a portion that is complementary or substantially complementary to an RBS.
38. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule represses translation by at least 80%.
39. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule represses translation by at least 90%.
40. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule represses translation by at least 98%.
41. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule has the sequence of crR10.
42. A DNA construct that comprises a template for transcription of the nucleic acid molecule of claim 41, wherein the nucleic acid molecule is composed of RNA.
43. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule has the sequence of crR12.
44. A DNA construct that comprises a template for transcription of the nucleic acid molecule of claim 43, wherein the nucleic acid molecule is composed of RNA.
45. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule is a variant of crR10 and differs from crR10 by 12 or less nucleotides and includes at least 3 dispersed areas of non-complementarity.

46. A DNA construct that comprises a template for transcription of the nucleic acid molecule of claim 45.
47. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule is a variant of crR12 and differs from crR12 by 12 or less nucleotides and includes at least 3 dispersed areas of non-complementarity.
48. A DNA construct that comprises a template for transcription of the nucleic acid molecule of claim 47, wherein the nucleic acid molecule is composed of RNA.
49. A DNA construct that comprises a template for transcription of the nucleic acid molecule of claim 1, wherein the nucleic acid molecule is composed of RNA.
50. A cell comprising the DNA construct of claim 49.
51. A transgenic non-human mammal comprising the DNA construct of claim 49.
52. A plasmid comprising the DNA construct of claim 49.
53. The plasmid of claim 52, wherein the plasmid comprises a promoter operably linked to the template for transcription of the nucleic acid molecule.
54. The plasmid of claim 53, wherein the promoter is inducible.
55. The plasmid of claim 53, wherein the promoter is synthetic.
56. The plasmid of claim 53, wherein the promoter is endogenous to a prokaryotic or eukaryotic cell.
57. The plasmid of claim 53, wherein the promoter is responsive to an environmental or developmental signal.
58. The plasmid of claim 53, wherein the promoter functions in prokaryotic cells.
59. The plasmid of claim 53, wherein the promoter functions in eukaryotic cells.
60. The plasmid of claim 52, wherein the nucleic acid molecule comprises a start codon and wherein the plasmid comprises a restriction site downstream of the template for transcription of the start codon.

61. A cell comprising the plasmid of claim 52.
62. An engineered nucleic acid molecule comprising:
 - (i) a first stem-forming portion;
 - (ii) a second stem-forming portion; and
 - (iii) a non-stem-forming portion, wherein the non-stem-forming portion connects the 3' end of the first stem-forming portion and the 5' end of the second stem-forming portion to form a loop,
and wherein a portion of the nucleic acid molecule is complementary or substantially complementary, to a portion of a cognate nucleic acid molecule of claim 1.
63. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule comprises a portion comprising the sequence YNAR positioned 5' to the 5' portion of the first stem-forming sequence.
64. The nucleic acid molecule of claim 62, wherein the length of the stem is between 6 and 50 nucleotides.
65. The nucleic acid molecule of claim 62, wherein the length of the stem is between 12 and 30 nucleotides.
66. The nucleic acid molecule of claim 62, wherein the length of the stem is approximately 19 nucleotides.
67. The nucleic acid molecule of claim 62, wherein the two stem-forming portions exhibit at least 66% complementarity.
68. The nucleic acid molecule of claim 62, wherein the two stem-forming portions exhibit between 75 and 95% complementarity.
69. The nucleic acid molecule of claim 62, wherein the two stem-forming portions exhibit approximately 85% complementarity.
70. The nucleic acid molecule of claim 62, wherein the stem includes at least one area of non-complementarity.

71. The nucleic acid molecule of claim 70, wherein the stem includes at least one bulge.
72. The nucleic acid molecule of claim 62, wherein the stem includes at least two dispersed areas of non-complementarity.
73. The nucleic acid molecule of claim 72, wherein the stem includes at least two dispersed bulges.
74. The nucleic acid molecule of claim 62, wherein the stem includes at least three dispersed areas of non-complementarity.
75. The nucleic acid molecule of claim 74, wherein the stem includes at least three dispersed bulges.
76. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule forms a single stem.
77. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule is composed of RNA.
78. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule is composed of DNA.
79. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule is composed of DNA and RNA.
80. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule comprises a nucleotide analog.
81. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule comprises a ligand binding domain.
82. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule activates translation of an mRNA whose translation is repressed by a cognate *cis*-repressive nucleic acid molecule.
83. The nucleic acid molecule of claim 82, wherein the nucleic acid molecule activates translation by at least 5 fold.

84. The nucleic acid molecule of claim 82, wherein the nucleic acid molecule activates translation by at least 10 fold.
85. The nucleic acid molecule of claim 82, wherein the nucleic acid molecule activates translation by at least 19 fold.
86. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule has the sequence of taR10.
87. A DNA construct that comprises a template for transcription of the nucleic acid molecule of claim 86, wherein the nucleic acid molecule is composed of RNA.
88. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule has the sequence of taR12.
89. A DNA construct that comprises a template for transcription of the nucleic acid molecule of claim 88, wherein the nucleic acid molecule is composed of RNA.
90. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule is a variant of taR10 and differs from taR10 by 12 or less nucleotides and includes at least 3 dispersed areas of non-complementarity.
91. A DNA construct that comprises a template for transcription of the nucleic acid molecule of claim 90, wherein the nucleic acid molecule is composed of RNA.
92. The nucleic acid molecule of claim 62, wherein the nucleic acid molecule is a variant of taR12 and differs from taR12 by 12 or less nucleotides and includes at least 3 dispersed areas of non-complementarity.
93. A DNA construct that comprises a template for transcription of the nucleic acid molecule of claim 92, wherein the nucleic acid molecule is composed of RNA.
94. A DNA construct that comprises a template for transcription of the nucleic acid molecule of claim 62, wherein the nucleic acid molecule is composed of RNA.
95. The DNA construct of claim 94, further comprising a template for transcription of the nucleic acid molecule of claim 1, wherein the nucleic acid molecule is composed of RNA.

96. A cell comprising the DNA construct of claim 94.
97. A transgenic non-human mammal comprising the DNA construct of claim 94.
98. A plasmid comprising the DNA construct of claim 94.
99. The plasmid of claim 98, wherein the plasmid comprises a promoter operably linked to the template for transcription of the nucleic acid molecule.
100. The plasmid of claim 98, wherein the promoter is inducible.
101. The plasmid of claim 98, wherein the promoter is synthetic.
102. The plasmid of claim 98, wherein the promoter is endogenous to a prokaryotic or eukaryotic cell.
103. The plasmid of claim 98, wherein the promoter is responsive to an environmental or developmental signal.
104. The plasmid of claim 98, wherein the promoter functions in prokaryotic cells.
105. The plasmid of claim 98, wherein the promoter functions in eukaryotic cells.
106. A cell comprising the plasmid of claim 98.
107. The plasmid of claim 98, further comprising the DNA construct of claim 49.
108. An engineered nucleic acid molecule comprising a sequence that is complementary or substantially complementary to a sequence located within a region comprising the 5' UTR of an mRNA and the first 20 nucleotides of the open reading frame, wherein the molecule represses translation of the open reading frame when positioned within the 5' UTR of the mRNA by forming a stem-loop structure with the sequence to which it is complementary or substantially complementary.
109. The nucleic acid molecule of claim 108, wherein the nucleic acid molecule comprises a YUNR sequence within a portion of the molecule that forms the loop in the stem-loop structure.

110. The nucleic acid molecule of claim 108, wherein the nucleic acid molecule comprises a sequence that is complementary or substantially complementary to an RBS.
111. The nucleic acid molecule of claim 108, wherein the nucleic acid molecule comprises a sequence that is complementary or substantially complementary to a Kozak consensus sequence.
112. An engineered nucleic acid molecule comprising:
- (i) a first stem-forming portion;
 - (ii) a second stem-forming portion, wherein the two stem-forming portions are complementary or substantially complementary, and wherein the second stem-forming portion comprises a 5' portion of an open reading frame and the first stem-forming portion comprises a portion that is complementary or substantially complementary to the 5' portion of the open reading frame;
 - (iii) a non-stem-forming portion that forms a loop connecting the 3' end of the first stem-forming portion and the 5' end of the second stem-forming portion, wherein the engineered nucleic acid molecule forms a stem-loop structure that represses translation of the open reading frame (ORF).
113. The nucleic acid molecule of claim 112, wherein the nucleic acid molecule comprises a YUNR sequence within the non-stem-forming portion.
114. The nucleic acid molecule of claim 112, wherein the first stem-forming portion comprises a sequence that is complementary or substantially complementary to an RBS.
115. The nucleic acid molecule of claim 112, wherein the first stem-forming portion comprises a sequence that is complementary or substantially complementary to a Kozak consensus sequence.
116. A system for control of gene expression comprising:

(i) a first nucleic acid molecule comprising a *cis*-repressive sequence element upstream of an open reading frame (ORF), wherein the first nucleic acid molecule forms a stem-loop structure that represses translation of the ORF; and

(ii) a second nucleic acid molecule comprising first and second stem-forming portions and a non-stem-forming portion, wherein the non-stem-forming portion connects the 3' end of the first stem-forming portion and the 5' end of the second stem-forming portion to form a loop, and wherein a portion of the second nucleic acid molecule is complementary or substantially complementary to a portion of the first nucleic acid molecule and interacts with the first nucleic acid molecule to derepress translation of the ORF.

117. The system of claim 116, wherein the first nucleic acid molecule represses translation by at least 80%.
118. The system of claim 116, wherein the first nucleic acid molecule represses translation by at least 90%.
119. The system of claim 116, wherein the first nucleic acid molecule represses translation by at least 98%.
120. The system of claim 116, wherein the second nucleic acid molecule activates translation by at least 5 fold.
121. The system of claim 116, wherein the second nucleic acid molecule activates translation by at least 10 fold.
122. The system of claim 116, wherein the second nucleic acid molecule activates translation by at least 19 fold.
123. The system of claim 116, wherein the first and second nucleic acid molecules are composed of RNA.
124. The system of claim 116, wherein the first and second nucleic acid molecules are composed of DNA.
125. The system of claim 116, wherein the first and second nucleic acid molecules are composed of DNA and RNA.

126. The system of claim 116, wherein the nucleic acid molecule is positioned upstream of the ORF.
127. The system of claim 116, wherein the first nucleic acid molecule comprises:
- (i) a first stem-forming portion;
 - (ii) a second stem-forming portion, wherein the two stem-forming portions are complementary or substantially complementary, and
 - (iii) a non-stem-forming portion that forms a loop connecting the 3' end of the first stem-forming portion and the 5' end of the second stem-forming portion, wherein the engineered nucleic acid molecule forms a stem-loop structure that represses translation when positioned upstream of an open reading frame (ORF).
128. The system of claim 127, wherein the first and second stem-forming portions are substantially complementary.
129. The system of claim 116, wherein at least a portion of the first nucleic acid molecule is complementary or substantially complementary to a ribosome binding site (RBS).
130. The system of claim 116, wherein at least a portion of the first nucleic acid molecule is complementary or substantially complementary to a Kozak consensus sequence.
131. The system of claim 127, wherein the sequence of the second stem-forming portion comprises an RBS.
132. The system of claim 127, wherein the sequence of the non-stem-forming portion comprises YUNR.
133. The system of claim 127, wherein the non-stem forming portion is 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides in length.
134. The system of claim 127, wherein the non-stem forming portion is between 13 and 50 nucleotides in length, inclusive.
135. The system of claim 116, wherein the length of the stem is between 4 and 100 nucleotides, inclusive.

136. The system of claim 116, wherein the length of the stem is between 6 and 50 nucleotides, inclusive.
137. The system of claim 116, wherein the length of the stem is between 12 and 30 nucleotides, inclusive.
138. The system of claim 116, wherein the length of the stem is approximately 19 nucleotides.
139. The system of claim 116, wherein the stem exhibits at least 66% complementarity.
140. The system of claim 116, wherein the stem exhibits between 75 and 95% complementarity.
141. The system of claim 116, wherein the stem exhibits approximately 85% complementarity.
142. The system of claim 116, wherein the stem includes at least one area of non-complementarity.
143. The system of claim 142, wherein the stem includes at least one bulge.
144. The system of claim 116, wherein the stem includes at least two dispersed areas of non-complementarity.
145. The system of claim 144, wherein the stem includes at least two dispersed bulges.
146. The system of claim 116, wherein the stem includes at least three dispersed areas of non-complementarity.
147. The system of claim 146, wherein the stem includes at least three dispersed bulges.
148. The system of claim 116, wherein the nucleic acid molecule forms a single stable stem.
149. The system of claim 116, wherein the nucleic acid molecule represses translation in the absence of a ligand.

150. The system of claim 116, wherein the first stem-forming portion comprises a sequence complementary or substantially complementary to a sequence in the 5' portion of an ORF.
151. The system of claim 127, wherein the nucleic acid molecule comprises a start codon.
152. The system of claim 151, wherein the nucleic acid molecule comprises a spacer comprising one or more nucleotides between the 3' end of the second stem-forming portion and the start codon.
153. The system of claim 151, wherein all or part of the start codon is located within the second stem-forming portion.
154. The system of claim 116, wherein the nucleic acid molecule comprises one or more nucleotides at the 5' end that do not participate in the stem-loop structure.
155. The system of claim 116, wherein the nucleic acid molecule comprises between 5 and 50 nucleotides upstream of the 5' end of the first stem-forming portion.
156. The system of claim 116, wherein the nucleic acid molecule comprises a ligand binding domain.
157. The system of claim 127, wherein the nucleic acid molecule comprises a third stem-forming portion that is complementary or substantially complementary to the second stem-forming portion, wherein the first and third stem-forming portions form alternate stem-loop structures with the second stem-forming portion.
158. The system of claim 157, wherein the first and third stem-forming portions comprise a portion that is complementary or substantially complementary to an RBS.
159. The system of claim 116, wherein the second nucleic acid molecule comprises a portion comprising the sequence YNAR positioned 5' to the 5' portion of the first stem-forming sequence.
160. The system of claim 116, wherein the length of the stem formed by the two stem-forming portions of the second nucleic acid molecule is between 6 and 50 nucleotides.

161. The system of claim 116, wherein the length of the stem formed by the two stem-forming portions of the second nucleic acid molecule is between 12 and 30 nucleotides.
162. The system of claim 116, wherein the length of the stem formed by the two stem-forming portions of the second nucleic acid molecule is approximately 19 nucleotides.
163. The system of claim 116, wherein the two stem-forming portions of the second nucleic acid molecule exhibit at least 66% complementarity.
164. The system of claim 116, wherein the two stem-forming portions of the second nucleic acid molecule exhibit between 75 and 95% complementarity.
165. The system of claim 116, wherein the two stem-forming portions of the second nucleic acid molecule exhibit approximately 85% complementarity.
166. The system of claim 116, wherein the stem formed by the two stem-forming portions of the second nucleic acid molecule includes at least one area of non-complementarity.
167. The system of claim 116, wherein the stem formed by the two stem-forming portions of the second nucleic acid molecule includes at least two dispersed areas of non-complementarity.
168. The system of claim 116, wherein the stem formed by the two stem-forming portions of the second nucleic acid molecule includes at least three dispersed areas of non-complementarity.
169. The system of claim 116, wherein the second nucleic acid molecule comprises a nucleotide analog.
170. The system of claim 116, wherein the second nucleic acid molecule comprises a ligand binding domain.

171. The system of claim 116, wherein the first and second nucleic acid molecules interact so as to disrupt the stem-loop structure formed by the first nucleic acid molecule, thereby allowing a ribosome to gain access to a ribosome binding site.
172. The system of claim 116, wherein the first nucleic acid molecule has the sequence of crR10 and the second nucleic acid molecule has the sequence of taR10.
173. The system of claim 116, wherein the first nucleic acid molecule has the sequence of crR12 and the second nucleic acid molecule has the sequence of taR12.
174. The system of claim 116, wherein the first nucleic acid molecule has the sequence of crR10 or a variant of crR10 that differs from crR10 by 12 nucleotides or less and includes at least 3 dispersed areas of non-complementarity and the second nucleic acid molecule has the sequence of taR10 or a variant of taR10 that differs from taR10 by 12 nucleotides or less and includes at least 3 dispersed areas of non-complementarity.
175. The system of claim 116, wherein the first nucleic acid molecule has the sequence of crR12 or a variant of crR12 that differs from crR12 by 12 nucleotides or less and includes at least 3 dispersed areas of non-complementarity and the second nucleic acid molecule has the sequence of taR12 or a variant of taR12 that differs from taR12 by 12 nucleotides or less and includes at least 3 dispersed areas of non-complementarity.
176. The system of claim 116, wherein the first nucleic acid molecule and the second nucleic acid molecule have an equilibrium association constant between 0.8×10^7 and 1.5×10^7 kcal/mol.
177. A kit for allowing a user to regulate expression of a gene of choice comprising:
- (a) a first plasmid comprising
 - (i) a template for transcription of a cis-repressive RNA element; and
 - (ii) a promoter located upstream of the template for transcription of the cis-repressive RNA element;
 - (b) a second plasmid comprising

- (i) a template for transcription of a cognate trans-activating RNA element; and
 - (ii) a promoter located upstream of the template for transcription of the trans-activating RNA element; and
 - (c) one or more elements selected from the list consisting of: (i) one or more inducers; (ii) host cells; (iii) one or more buffers; (iv) an enzyme, e.g., a restriction enzyme; (v) DNA isolation reagents; (vi) DNA purification reagents; (vii) a control plasmid lacking a crRNA or taRNA sequence; (viii) a control plasmid containing a crRNA or taRNA sequence or both; (ix) sequencing primers; and (x) instructions for use.
178. A kit for allowing a user to regulate expression of a gene of choice comprising:
a plasmid comprising a template for transcription of a cis-repressive RNA element and a promoter located upstream of the template for transcription of the cis-repressive RNA element and further comprising a template for transcription of a cognate trans-activating RNA element and a promoter located upstream of the template for transcription of the cognate trans-activating RNA element; and
one or more elements selected from the list consisting of: (i) one or more inducers; (ii) host cells; (iii) one or more buffers; (iv) an enzyme, e.g., a restriction enzyme; (v) DNA isolation reagents; (vi) DNA purification reagents; (vii) a control plasmid lacking a crRNA or taRNA sequence; (viii) a control plasmid containing a crRNA or taRNA sequence or both; (ix) sequencing primers; and (x) instructions for use.
179. A kit for allowing a user to regulate expression of a gene of choice comprising:
- (a) a first plasmid comprising
 - (i) a template for transcription of a cis-repressive RNA element; and
 - (ii) a promoter located upstream of the template for transcription of the cis-repressive RNA element;
 - (b) a second plasmid comprising
 - (i) a template for transcription of a cognate trans-activating RNA element; and
 - (ii) a promoter located upstream of the template for transcription of the trans-activating RNA element;

(c) a third plasmid comprising a template for transcription of a cis-repressive RNA element and a promoter located upstream of the template for transcription of the cis-repressive RNA element and further comprising a template for transcription of a cognate trans-activating RNA element and a promoter located upstream of the template for transcription of the cognate trans-activating RNA element; and

(d) one or more elements selected from the list consisting of: (i) one or more inducers; (ii) host cells; (iii) one or more buffers; (iv) an enzyme, e.g., a restriction enzyme; (v) DNA isolation reagents; (vi) DNA purification reagents; (vii) a control plasmid lacking a crRNA or taRNA sequence; (viii) a control plasmid containing a crRNA or taRNA sequence or both; (ix) sequencing primers; and (x) instructions for use.

180. A kit comprising

one or more oligonucleotides comprising a crRNA sequence, one or more oligonucleotides comprising a taRNA sequence, or one or more oligonucleotides comprising a crRNA sequence and one or more oligonucleotides comprising a taRNA sequence, wherein the kit further comprises one or more items selected from the group consisting of: (i) one or more inducers; (ii) host cells; (iii) one or more buffers; (iv) an enzyme, e.g., a restriction enzyme; (v) DNA isolation reagents; (vi) DNA purification reagents; (vii) a control plasmid lacking a crRNA or taRNA sequence; (viii) a control plasmid containing a crRNA or taRNA sequence or both; (ix) sequencing primers; and (x) instructions for use.

181. A method of regulating translation of an open reading frame comprising:

introducing an engineered template for transcription of an mRNA into a cell and allowing mRNA transcription to occur resulting in a transcribed mRNA, wherein the template is engineered so that the transcribed mRNA comprises first and second nucleic acid elements that form a stem-loop structure that represses translation of the mRNA; and

providing an engineered nucleic acid molecule that interacts with the mRNA so as to derepress translation of the mRNA to the cell.

182. The method of claim 181, wherein the engineered template comprises:

(i) a first stem-forming portion:

(ii) a second stem-forming portion, wherein the two stem-forming portions are complementary or substantially complementary, and

(iii) a non-stem-forming portion that forms a loop connecting the 3' end of the first stem-forming portion and the 5' end of the second stem-forming portion, wherein the engineered nucleic acid molecule forms a stem-loop structure that represses translation when positioned upstream of an open reading frame (ORF).

183. The method of claim 182, wherein the first and second stem-forming portions are substantially complementary.
184. The method of claim 182, wherein at least a portion of the first stem-forming portion is complementary or substantially complementary to a ribosome binding site .
185. The method of claim 182, wherein at least a portion of the first stem-forming portion is complementary or substantially complementary to a Kozak consensus sequence.
186. The method of claim 182, wherein the sequence of the second stem-forming portion comprises an RBS.
187. The method of claim 182, wherein the sequence of the non-stem-forming portion comprises YUNR.
188. The method of claim 182, wherein the non-stem forming portion is 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides in length.
189. The method of claim 182, wherein the non-stem forming portion is between 13 and 50 nucleotides in length, inclusive.
190. The method of claim 182, wherein the length of the stem is between 4 and 100 nucleotides, inclusive.
191. The method of claim 182, wherein the length of the stem is between 6 and 50 nucleotides, inclusive.
192. The method of claim 182, wherein the length of the stem is between 12 and 30 nucleotides, inclusive.

193. The method of claim 182, wherein the length of the stem is approximately 19 nucleotides.
194. The method of claim 182, wherein the stem exhibits at least 66% complementarity.
195. The method of claim 182, wherein the stem exhibits between 75 and 95% complementarity.
196. The method of claim 182, wherein the stem exhibits approximately 85% complementarity.
197. The method of claim 182, wherein the stem includes at least one area of non-complementarity.
198. The method of claim 197, wherein the stem includes at least one bulge.
199. The method of claim 182, wherein the stem includes at least two dispersed areas of non-complementarity.
200. The method of claim 199, wherein the stem includes at least two dispersed bulges.
201. The method of claim 182, wherein the stem includes at least three dispersed areas of non-complementarity.
202. The method of claim 201, wherein the stem includes at least three dispersed bulges.
203. The method of claim 182, wherein the first stem-forming portion comprises a sequence complementary or substantially complementary to a sequence in the 5' portion of an ORF.
204. The method of claim 182, wherein the transcribed mRNA comprises a start codon and a spacer comprising one or more nucleotides between the 3' end of the second stem-forming portion and the start codon.
205. The method of claim 204, wherein all or part of the start codon is located within the second stem-forming portion.

206. The method of claim 182, wherein the transcribed mRNA comprises one or more nucleotides upstream of the 5' end of the first stem-forming portion.
207. The method of claim 182, wherein the transcribed mRNA comprises between 5 and 50 nucleotides upstream of the 5' end of the first stem-forming portion.
208. The method of claim 182, wherein the transcribed mRNA further comprises a third stem-forming portion that is complementary or substantially complementary to the second stem-forming portion, wherein the first and third stem-forming portions form alternate stem-loop structures with the second stem-forming portion.
209. The method of claim 208, wherein the first and third stem-forming portions comprise a portion that is complementary or substantially complementary to an RBS.
210. The method of claim 181, wherein the step of providing comprises:
inducing transcription of the engineered nucleic acid molecule in the cell.
211. The method of claim 181, wherein the step of providing comprises:
delivering the engineered nucleic acid molecule exogenously.
212. The method of claim 181, wherein the engineered nucleic acid molecule comprises:
(i) a first stem-forming portion;
(ii) a second stem-forming portion; and
(iii) a non-stem-forming portion, wherein the non-stem-forming portion connects the 3' end of the first stem-forming portion and the 5' end of the second stem-forming portion to form a loop,
and wherein a portion of the nucleic acid molecule is complementary or substantially complementary, to a portion of the transcribed mRNA.
213. The method of claim 212, wherein the nucleic acid molecule comprises a portion comprising the sequence YNAR positioned 5' to the 5' portion of the first stem-forming sequence.
214. The method of claim 212, wherein the length of the stem is between 4 and 100 nucleotides, inclusive.

- 215. The method of claim 212, wherein the length of the stem is between 6 and 50 nucleotides, inclusive.
- 216. The method of claim 212, wherein the length of the stem is between 12 and 30 nucleotides, inclusive.
- 217. The method of claim 212, wherein the length of the stem is approximately 19 nucleotides.
- 218. The method of claim 212, wherein the two stem-forming portions exhibit at least 66% complementarity.
- 219. The method of claim 212, wherein the two stem-forming portions exhibit between 75 and 95% complementarity.
- 220. The method of claim 212, wherein the two stem-forming portions exhibit approximately 85% complementarity.
- 221. The method of claim 212, wherein the stem includes at least two dispersed areas of non-complementarity.
- 222. The method of claim 221, wherein the stem includes at least two dispersed bulges.
- 223. The method of claim 212, wherein the stem includes at least three dispersed areas of non-complementarity.
- 224. The method of claim 223, wherein the stem includes at least three dispersed bulges.
- 225. The method of claim 212, wherein the nucleic acid molecule forms a single stem.
- 226. The method of claim 181, wherein the nucleic acid molecule is composed of RNA.
- 227. The method of claim 181, wherein the nucleic acid molecule is composed of DNA.
- 228. The method of claim 181, wherein the nucleic acid molecule is composed of DNA and RNA.
- 229. The method of claim 181, wherein the nucleic acid molecule comprises a nucleotide analog.

230. The method of claim 181, wherein the nucleic acid molecule comprises a ligand binding domain.
231. The method of claim 181, wherein the first nucleic acid molecule has the sequence of crR10 and the second nucleic acid molecule has the sequence of taR10.
232. The method of claim 181, wherein the first nucleic acid molecule has the sequence of crR12 and the second nucleic acid molecule has the sequence of taR12.
233. The method of claim 181, wherein the first nucleic acid molecule has the sequence of crR10 or a variant of crR10 that differs from crR10 by 12 nucleotides or less and includes at least 3 dispersed areas of non-complementarity and the second nucleic acid molecule has the sequence of taR10 or a variant of taR10 that differs from taR10 by 12 nucleotides or less and includes at least 3 dispersed areas of non-complementarity.
234. The method of claim 181, wherein the first nucleic acid molecule has the sequence of crR12 or a variant of crR12 that differs from crR12 by 12 nucleotides or less and includes at least 3 dispersed areas of non-complementarity and the second nucleic acid molecule has the sequence of taR12 or a variant of taR12 that differs from taR12 by 12 nucleotides or less and includes at least 3 dispersed areas of non-complementarity.
235. The method of claim 181, wherein the first nucleic acid molecule and the second nucleic acid molecule have an equilibrium association constant between 0.8×10^7 and 1.5×10^7 kcal/mol.
236. A method of analyzing gene expression comprising:
- (i) repressing translation of an mRNA transcribed from a gene of interest using a *cis*-repressive RNA element;
 - (ii) measuring expression of one or more genes;
 - (iii) activating translation of the mRNA using a cognate *trans*-activating RNA element; and
 - (iv) measuring expression of the one or more genes of step (ii).

237. The method of claim 236, wherein the steps of measuring gene expression comprise obtaining a gene expression profile using a microarray.
238. A method of selecting a cognate pair of nucleic acid molecules for regulating translation comprising steps of:
- (i) providing one or more starting nucleic acid sequences;
 - (ii) randomizing the sequence or sequences to generate one or more pools of randomized nucleic acid sequences; and
 - (iii) employing *in vitro* selection to identify a candidate cognate nucleic acid pair comprising a repressive element that represses translation when positioned upstream of an ORF and an activating element that derepresses translation that is repressed by the candidate repressive element.
239. The method of claim 238, further comprising the step of:
- (i) testing the repressive element by inserting it upstream of an open reading frame and measuring translation; or
 - (ii) testing the activating element by determining whether it derepresses translation that is repressed by the repressive element; or
 - (iii) performing both (i) and (ii).
240. The method of claim 238, wherein the one or more nucleotide sequences are provided as DNA.
241. A method of selecting a cognate pair of nucleic acid molecules for regulating translation comprising steps of:
- (i) providing a starting sequence of a crRNA:taRNA cognate pair; and
 - (ii) making one or more nucleotide additions, deletions, or substitutions in either or both sequences, such that the overall percentage of complementarity in the crRNA stem, the taRNA stem, and the crRNA:taRNA duplex remain within 10% of their starting values and the number of dispersed areas of non-complementarity in the crRNA stem, the taRNA stem, and the crRNA:taRNA duplex remain the same as their starting values.
242. A collection of cognate *cis*-repressive and *trans*-activating nucleic acid molecule pairs.